180

182

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SEQUENCE LISTING

110> Duvick, Jonathan P. Gilliam, Jacob T. Maddox, Joyce R.

Amino Polyol Amine Oxidase

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Polynucleotides and Related Polypeptides and Methods of Use
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					aca Thr											336
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					ctc Leu											624
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gta Val 305	tgg Trp	gac Asp	aag Lys	ccg Pro	tgg Trp 310	tgg Trp	cgc Arg	gaa Glu	caa Gln	ggc Gly 315	ttc Phe	tcg Ser	ggc Gly	gtc Val	ctc Leu 320	960	
caa Gln	tcg Ser	agc Ser	tgt Cys	gac Asp 325	ccc Pro	atc Ile	tca Ser	ttt Phe	gcc Ala 330	aga Arg	gat Asp	acc Thr	agc Ser	atc Ile 335	gac Asp	1008	
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	caa Gln 370															1152	
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caa Gln	cga Arg 450	ggt Gly	gct Ala	gca Ala	gaa Glu	gtt Val 455	gtg Val	gct Ala	agc Ser	ctg Leu	gtg Val 460	cca Pro	gca Ala	gca Ala		1389	
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							ctc Leu 190										864
							gac Asp										912
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							ctc Leu										1008
							gta Val										1056
							tcg Ser 270										1104
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							ttc Phe										1248
	ccc Pro	atc Ile	tca Ser 330	ttt Phe	gcc Ala	aga Arg	gat Asp	acc Thr 335	agc Ser	atc Ile	gac Asp	gtc Val	gat Asp 340	cga Arg	caa Gln	tgg Trp	1296
							gtc Val 350										1344
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,	gcc Ala	tac Tyr	gag Glu	aac Asn	gcc Ala 380	gly aaa	gcc Ala	caa Gln	gtc Val	cca Pro 385	gag Glu	ccg Pro	gcc Ala	aac Asn	gtg Val 390	ctc Leu	1440
							cag Gln										1488
•	gtc Val	tat Tyr	gly aaa	ctg Leu	aac Asn	gat Asp	ctc Leu	atc Ile	aca Thr	ctg Leu	ggt Gly	tcg Ser	gcg Ala	ctc Leu	aga Arg	acg Thr	1536

415 420 410 1584 ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp 435 430 aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca 1632 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala 445 450 gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c 1673 Glu Val Val Ala Ser Leu Val Pro Ala Ala 460 <210> 17 <211> 554 <212> PRT <213> Exophiala spinifera <220> <221> SIGNAL <222> (1)...(89) <400> 17 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser -80 -85 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln -60 -70 -65 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe -50 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -35 -30 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val -15 -20 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala -5 1 Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 15 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 45 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 75 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 95 Thr Ala Pro Tyr Gly Asp Sér Leu Leu Ser Glu Glu Val Ala Ser Ala 110 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 125 130 Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 160 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 175 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly 190

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Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
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Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
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Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
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                    285
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
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	_		_			aaa Lys	_	-								384
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						cct Pro										480
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						att Ile										576
						ata Ile										624
						cat His 215										672
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						gag Glu										768

				245					250					255		
_		_		_	ctt Leu			_	_	_	_			_		816
_	_	_		_	ggt Gly				_				_			864
					gac Asp											912
					gag Glu 310											960
			_		gac Asp						_				_	1008
	_	_	_		gag Glu	_	_	_	_							1056
-			_	_	atc Ile	-			_			_		-		1104
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					aag Lys											1296
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-	_	_	_	_	ggc Gly	_			_	_		_			_	1488

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ccc gcc gag Pro Ala Glu 515												1584
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gat acc agc Asp Thr Ser												1728
gtc gga gac Val Gly Asp												1776
caa aag tct Gln Lys Ser 595												1824
gcc caa gtc Ala Gln Val 610			. Asn									1872
cag cag tat Gln Gln Tyr 625												1920
ctc atc aca Leu Ile Thr												1968
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Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
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Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
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Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
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Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
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Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
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      residue; nucleotides 76 -1464 , trAPAO cDNA.
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48

						agc Ser										96
			_		_	agc Ser 15		_		_	-	_			_	144
						ctc Leu										192
						caa Gln										240
_			-			atc Ile		_	-			_	_	-		288
						cat His										336
						gca Ala 95		_						_		384
		_		_	_	agc Ser			_	_	-	-			-	432
			_			cag Gln	_		-			_			-	480
	_		-		_	gcg Ala	_			_	_		_			528
		_		_	_	cta Leu		_		-	-			_	_	576
						ctg Leu 175										624
_					_	tac Tyr		_	_	_				_		672
		_	_	_		gac Asp			_		_					720
	_	_	_		_	cat His	_	_		_	-		_			768
						ccc Pro	_	-	-			_	_	_		816

		235					240					245			
					tcg Ser										864
		-	_		ccg Pro 270			_				_			912
					gag Glu										960
			_	_	ata Ile	_		_		_	_	_		 _	1008
_				-	ggc Gly	_			_	_	_	_			1056
					agc Ser										1104
					gac Asp 350										1152
					tct Ser										1200
					gtc Val										1248
	_	-	_	_	tat Tyr				~	_	_	_	_		1296
					aca Thr										1344
					gga Gly 430										1392
					cga Arg										1440
					gca Ala		tag		·						1464

<210> 21 <211> 487 <212> PRT

<213> Unknown

<220>

<221> SIGNAL

<222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize.

<400> 21 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly -20 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val -5 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln 15 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly 30 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn 50 45 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro 100 Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu 115 110 Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp 130 125 Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala 145 His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala 160 Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser 180 1.75 Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn 195 190 Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr 210 205 Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly 225 220 Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser 240 245 Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys 260 255 Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser 275 270 Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu 290 285 Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg 31.0 305 300 Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser 325 320 Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr 340 335 Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys 350 355 Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu 370

Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu

			380)				385	5				390)		
		395	5				400)				405	Val	. Туг	Gly	
Let	Asr 410		Leu	ıle	Thr	Leu 415		/ Ser	Ala	Let	420		Pro	Phe	Lys	
Ser 425	Val	. His	Phe	val	Gly 430		Glu	Thr	Ser	Leu 435		. Trp	Lys	Gly	Tyr 440	
Met	Glu	ı Gly	⁄ Ala	1le 445		Ser	Gly	Gln Gln	Arg	r Gly		Ala	Glu	Val	Val	
Ala	Ser	Leu	Val 460	Pro	Ala	Ala			130					400	'	
<21 <21	0> 2 1> 1 2> D 3> E	E08.	iala	spi	nife	ra										
<220> <221> CDS <222> (1)(1800)																
	0> 2		. (20	00,												
atg	gca	ctt	gca Ala	ccg Pro 5	agc Ser	tac Tyr	atc Ile	aat Asn	ccc Pro 10	cca Pro	aac Asn	gtc Val	gcc Ala	tcc Ser 15	cca Pro	48
gca Ala	gl ^a aaa	tat Tyr	tct Ser 20	cac His	gtc Val	ggc Gly	gta Val	ggc Gly 25	cca Pro	gac Asp	gga Gly	gly aaa	agg Arg 30	tat Tyr	gtg Val	96
aca Thr	ata Ile	gct Ala 35	gga Gly	cag Gln	att Ile	gga Gly	caa Gln 40	gac Asp	gct Ala	tcg Ser	ggc	gtg Val 45	aca Thr	gac Asp	cct Pro	144
gcc Ala	tac Tyr 50	gag Glu	aaa Lys	cag Gln	gtt Val	gcc Ala 55	caa Gln	gca Ala	ttc Phe	gcc Ala	aat Asn 60	ctg Leu	cga Arg	gct Ala	tgc Cys	192
ctt Leu 65	gct Ala	gca Ala	gtt Val	gga Gly	gcc Ala 70	act Thr	tca Ser	aac Asn	gac Asp	gtc Val 75	acc Thr	aag Lys	ctc Leu	aat Asn	tac Tyr 80	240
tac Tyr	atc Ile	gtc Val	gac Asp	tac Tyr 85	gcc Ala	ccg Pro	agc Ser	aaa Lys	ctc Leu 90	acc Thr	gca Ala	att Ile	gga Gly	gat Asp 95	gly aaa	288
ctg Leu	aag Lys	gct Ala	acc Thr 100	ttt Phe	gcc Ala	ctt Leu	gac Asp	agg Arg 105	ctc Leu	cct Pro	cct Pro	tgc Cys	acg Thr 110	ctg Leu	gtg Val	336
cca Pro	gtg Val	tcg Ser 115	gcc Ala	ttg Leu	tct Ser	tca Ser	cct Pro 120	gaa Glu	tac Tyr	ctc Leu	ttt Phe	gag Glu 125	gtt Val	gat Asp	gcc Ala	384
acg Thr	gcg Ala 130	ctg Leu	gtg Val	ccg Pro	gga Gly	cac His 135	acg Thr	acc Thr	cca Pro	gac Asp	aac Asn 140	gtt Val	gcg Ala	gac Asp	gtg Val	432
gta Val 145	gtg Val	gtg Val	ggc Gly	gct Ala	ggc Gly 150	ttg Leu	agc Ser	ggt Gly	ttg Leu	gag Glu 155	acg Thr	gca Ala	cgc Arg	aaa Lys	gtc Val 160	480

		ggt Gly			_		_				_	_	_	_	528
	-	act Thr 180	_	_	_		_					_			576
		ggc	_					_	_			_	_	_	624
		ttt Phe													672
		tca Ser				_		_						-	720
		 gac Asp		_	_	_			_	_	_	-			768
-		ccc Pro 260	_			_	_		_			_			816
		gcg Ala	_		_		_			_	_		_		864
		tgt Cys		_	_			_		_	_			_	912
		atc Ile													960
		ttt Phe		Thr		Tyr	Ile	Lys	Ser						1008
		tcg Ser 340													1056
		cag Gln													1104
		cac His													1152
		aca Thr													1200
		gtt Val													1248

	405	410		415
	Pro Ala Glu L		ttg gcg gaa aat Leu Ala Glu Asn 430	
	Ser Lys Ile V	_	tgg gac aag ccg Trp Asp Lys Pro 445	
			tcg agc tgt gac Ser Ser Cys Asp 460	
	-		gat cga caa tgg Asp Arg Gln Trp 475	
			aag tgg tcc caa Lys Trp Ser Gln	=
	Gln Lys Ser V		caa ctc cgc gca Gln Leu Arg Ala 510	- <u>-</u>
	Ala Gln Val P		gcc aac gtg ctc Ala Asn Val Leu 525	
			gct ccg agc gcc Ala Pro Ser Ala 540	
			gcg ctc aga acg Ala Leu Arg Thr 555	
0 0 0			tct tta gtt tgg Ser Leu Val Trp	
	Ala Ile Arg S		cga ggt gct gca Arg Gly Ala Ala 590	
gtg gct agc ctg Val Ala Ser Leu 595	Val Pro Ala A			1803
<210> 23 <211> 600 <212> PRT <213> Exophiala	spinifera			
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1 Ala Gly Tyr Ser 20	5 His Val Gly V	10 Val Gly Pro 25	Asp Gly Gly Arg	15 Tyr Val
	Gln Ile Gly G		Ser Gly Val Thr	Asp Pro

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr

```
540
                        535
  530
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
                    550
                                         555
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                565
                                     570
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
                                585
            580
Val Ala Ser Leu Val Pro Ala Ala
        595
<210> 24
<211> 3003
<212> DNA
<213> Unknown
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<223> Sequence is barley alpha amylase signal sequence:
      esp1 mat: an artificial spacer sequence and
      K:trAPAO
<221> sig peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence
<221> misc_feature
<222> (73)...(1575)
<223> esp1 mat
<221> misc feature
<222> (1576) ... (1611)
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<223> K:trAPAO
<221> CDS
<222> (1) ... (3000)
<221> misc feature
<222> (1612)...(1614)
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                                                                       48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
                -20
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct
                                                                        96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
ggg atg gtg gtc ggc acg act act gtc ccc ggc acc act gcg acc
                                                                       144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
                         15
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt
                                                                       192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
                     30
                                                                       240
```

geg cet cet act egt eee gtg eet tgg tea acg eet ttg eaa gee act

Ala	Pro	Pro	Thr	Arg 45	Pro	Val	Pro	Trp	Ser 50	Thr	Pro	Leu	Gln	Ala 55	Thr		
_				_	_						tac Tyr		-	_		2	88
_			_	_	_					_	ccc Pro	_		_		3	36
_	_		_	_	_						gtc Val 100					3	84
											ggt Gly					4	32
									-		gct Ala	_		_	_	4	80
											aga Arg					5	28
											cag Gln					5	76
											cag Gln 180					6	24
											ttt Phe					6	72
		_	_	_	Asp	Val	Leu	_	Thr		atg Met					7:	20
		_	-	_		_	_			~ ~	gct Ala					7(68
											act Thr					8:	16
											atg Met 260					86	64
											gga Gly					9:	12
											tct Ser					96	60

_			_		gct Ala	_	_		-				_		-	1008
					ttt Phe											1056
			_		ccg Pro		_		_			_				1104
					gga Gly 350											1152
					acc Thr											1200
	_	_	_		cgg Arg								~			1248
					gag Glu											1296
		_		_	gtc Val		_				_			_	_	1344
_			_	-	gag Glu 430	_	_	_	_			-	_		_	1392
		_		_	aaa Lys			_								1440
					gcg Ala											1488
_	_				aca Thr		_		_	-	-	-				1536
			_	_	ggc Gly				_							1584
				_	ggc Gly 510			-		_						1632
_	_	-		-	ggc Gly	_	_		_		_	_	_		_	1680
cag	gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	1728

Gln	Ala	Ala	Gly 540	Leu	Ser	Cys	Leu	Val 545	Leu	Glu	Ala	Met	Asp 550	Arg	Val		
				ctg Leu												1	.776
aac Asn	gac Asp 570	ctc Leu	gly	gct Ala	gcg Ala	tgg Trp 575	atc Ile	aat Asn	gac Asp	agc Ser	aac Asn 580	caa Gln	agc Ser	gaa Glu	gta Val	1	824
				gaa Glu												1	872
				atc Ile 605												1	920
cct Pro	tat Tyr	ggt Gly	gac Asp 620	tcc Ser	ttg Leu	ctg Leu	agc Ser	gag Glu 625	gag Glu	gtt Val	gca Ala	agt Ser	gca Ala 630	ctt Leu	gcg Ala	1	.968
gaa Glu	ctc Leu	ctc Leu 635	ccc Pro	gta Val	tgg Trp	tct Ser	cag Gln 640	ctg Leu	atc Ile	gaa Glu	gag Glu	cat His 645	agc Ser	ctt Leu	caa Gln	2	2016
				agc Ser												2	2064
				gag Glu												2	2112
				aca Thr 685												2	2160
				ctc Leu												2	2208
				gac Asp												2	2256
				tcg Ser												2	2304
				ctc Leu												2	2352
				gta Val 765												2	2400
				tcg Ser												2	2448

tca co Ser Pr	ro	cct Pro 795	ctt Leu	ccc Pro	gcc Ala	gag Glu	aag Lys 800	caa Gln	gca Ala	ttg Leu	gcg Ala	gaa Glu 805	aat Asn	tct Ser	atc Ile	2496
ctg gg Leu G 8:																2544
cgc ga Arg G 825	aa lu	caa Gln	ggc Gly	ttc Phe	tcg Ser 830	ggc Gly	gtc Val	ctc Leu	caa Gln	tcg Ser 835	agc Ser	tgt Cys	gac Asp	ccc Pro	atc Ile 840	2592
tca ti Ser Pl	tt he	gcc Ala	aga Arg	gat Asp 845	acc Thr	agc Ser	atc Ile	gac Asp	gtc Val 850	gat Asp	cga Arg	caa Gln	tgg Trp	tcc Ser 855	att Ile	2640
acc to																2688
aag ca Lys G																2736
gag a Glu A 8	ac sn	gcc Ala	Gly 333	gcc Ala	caa Gln	gtc Val 895	cca Pro	gag Glu	ccg Pro	gcc Ala	aac Asn 900	gtg Val	ctc Leu	gaa Glu	atc Ile	2784
gag te Glu T 905	gg 'rp	tcg Ser	aag Lys	cag Gln	cag Gln 910	tat Tyr	ttc Phe	caa Gln	gga Gly	gct Ala 915	ccg Pro	agc Ser	gcc Ala	gtc Val	tat Tyr 920	2832
gly r	tg eu	aac Asn	gat Asp	ctc Leu 925	atc Ile	aca Thr	ctg Leu	ggt Gly	tcg Ser 930	gcg Ala	ctc Leu	aga Arg	acg Thr	ccg Pro 935	ttc Phe	2880
aag a																2928
tat a Tyr M	itg Iet	gaa Glu 955	gly aaa	gcc Ala	ata Ile	cga Arg	tcg Ser 960	ggt Gly	caa Gln	cga Arg	ggt Gly	gct Ala 965	gca Ala	gaa Glu	gtt Val	2976
gtg g Val A 9								tag								3003
<210><211><212><213>	• 10 • PR	000 RT	wn												·	
<221>	<220> <221> SIGNAL <222> (1)(24)															

<223> Barley alpha amylase signal sequence: esp1 mat: an artifical spacer and k:trAPAO

<400> 25 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly -20 -15 Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr 15 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe 30 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr 45 50 Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly 80 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu 115 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala 130 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu 145 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly 160 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala 175 180 Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala 190 195 Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro 210 Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe 225 Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu 240 245 Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp 255 260 Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu 270 275 Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg 285 290 Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala 305 Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr 320 325 Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu 335 340 Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln 350 355 Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile 365 370 Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr 385 Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val 400 Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala 415 420 Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala 435 Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln 450 Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val

465 Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg 480 Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly 495 Ser Gly Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val 510 515 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 545 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 560 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 575 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 590 595 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 605 610 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 625 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 655 Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 670 675 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 705 Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 720 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 735 Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 750 755 Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 770 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 785 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 800 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 815 820 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 830 835 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 845 850 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 865 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 880 885 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 895 900 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 910 915 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 925 930 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 945 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val

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Val Ala Ser Leu Val Pro Ala Ala
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<210> 26
<211> 2976
<212> DNA
<213> Unknown
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      mature: artificial spacer: and K:trAPAO. For
      plant expression.
<221> sig peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence
<221> mat peptide
<222> (73)...(1545)
<223> BEST1 mature
<221> misc feature
<222> (1546)...(1584)
<223> spacer sequence
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<223> K:trAPAO
<221> CDS
<222> (1)...(2973)
<221> misc feature
<222> (1585)...(1587)
<223> Extra lysine
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                                                                        48
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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
                -20
ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc
                                                                        96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
             - 5
                                 1
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc
                                                                       144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
     10
                          15
                                                                       192
gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt
                                                                       240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
                                      50
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc
                                                                       288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
             60
                                  65
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ggc Gly	gct Ala 90	aaa Lys	ccc Pro	ggc	cag Gln	tac Tyr 95	ccc Pro	gtc Val	atg Met	gtc Val	tgg Trp 100	gtc Val	tac Tyr	ggc Gly	ggc Gly	384
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Val Trp Asp	Lys Pro Tr	Trp Arg G	**	Phe Ser Gly 820	Val Leu
caa tcg agc Gln Ser Ser 825		lle Ser Ph			
gtc gat cga Val Asp Arg					
cgg aag tgg Arg Lys Trp		Ser Lys G			
gac caa ctc Asp Gln Leu 875					
ccg gcc aac Pro Ala Asn 890					
gga gct ccg Gly Ala Pro 905		Tyr Gly Le			
tcg gcg ctc Ser Ala Leu	aga acg ccg Arg Thr Pro 925	ttc aag ag Phe Lys Se	gt gtt cat er Val His 930	ttc gtt gga Phe Val Gly	acg gag 2880 Thr Glu 935
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Leu Ser Ala	-20		-15		-10
	-5	- :	1	5	
10 Gly Ile Pro		15		20	
	<u>.</u>		2 2	5 1	=

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val

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Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
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Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
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Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
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                            880
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg
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Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa
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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
                                                                       240
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
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120

125

384

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					atc Ile											1152

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								tct Ser								1872

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ggt Gly act Thr 785	Ala ctg Leu 770 ctg Leu	Gly 755 tcc Ser agc Ser	tgc Cys gta Val	Ser ctc Leu caa Gln	gtt Val tcg Ser 790	ctt Leu 775 ggt Gly	Glu 760 gag Glu ccc Pro	Thr gcg Ala ggc Gly	Ala atg Met agg Arg	Arg gat Asp acg Thr 795	cgt Arg 780 act Thr	Val 765 gta Val atc Ile	ggg Gly aac Asn	Ala gga Gly gac	Ala aag Lys ctc Leu 800 ttg	€ 2352
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atc aca cgc gct ctg Ile Thr Arg Ala Leu 915	ctc ggt gtg gaa go Leu Gly Val Glu Al 920	cc cac gag atc agc atc la His Glu Ile Ser Met 925	ctt 2784 Leu
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cag tcg att tgc cat Gln Ser Ile Cys His 965	Ala Met Ser Lys G	aa ctt gtt cca ggc tca lu Leu Val Pro Gly Sen 70 97!	. Val
cac ctc aac acc ccc His Leu Asn Thr Pro 980	gtc gct gaa att ga Val Ala Glu Ile G 985	ag cag tcg gca tcc ggo lu Gln Ser Ala Ser Gly 990	c tgt 2976 7 Cys
aca gta cga tcg gcc Thr Val Arg Ser Ala 995	tog ggc gcc gtg t Ser Gly Ala Val Pl 1000	tc cga agc aaa aag gtg he Arg Ser Lys Lys Va 1005	g gtg 3024 L Val
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aga gat acc agc atc Arg Asp Thr Ser Ile 1075	c gac gtc gat cga c Asp Val Asp Arg G 1080	aa tgg tcc att acc tg ln Trp Ser Ile Thr Cy 1085	t ttc 3264 s Phe
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cga caa aag tct gto Arg Gln Lys Ser Val 1105	c tgg gac caa ctc c l Trp Asp Gln Leu A 1110	gc gca gcc tac gag aa rg Ala Ala Tyr Glu As 1115	c gcc 3360 n Ala 1120

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1125 1130 1135	
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gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val 1155 1160 1165	3504
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu 1170 1175 1180	3552
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Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala
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Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys
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Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly
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       835
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Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys
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Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln
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Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe
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His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
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Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
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Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
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His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
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Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
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tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac
                                                                       240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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gtt tgt tt Val Cys Ph		_		Ile Pro		-		576
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acg ttt gg Thr Phe Gl 210								672
gga tcc cc Gly Ser Pr 225			_	-	g Arg Thr			720
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tat gca gc Tyr Ala Al		Val Gly		Arg Tr	o Lys Pro			816
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tgc ttc gg Cys Phe Gl 290								912
agc gag ga Ser Glu As 305					a Pro Ser			960
ccc ggc ca Pro Gly Gl	=*	Val Met		-			Ala	1008
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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
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1800

1860 1920

1929

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taatattqtc tcqqacaaqa aaqacggcgg gcagtatatg cgatgcaaaa cagqtgcgtg
                                                                      1140
cggtgtcctc tcaggtaggg gactcgtttc ttagtggtca ttccaggtat gcagtcgatt
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                                                                      1260
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ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcgggcgc cgtgttccga
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1440 1500

1560 1620

1680

1740

1800

1860

1920 1929

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Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
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Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
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Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
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                                     90
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
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Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
                                                 125
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                                             140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
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Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
                                                 205
                            200
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Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
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Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
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Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
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Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
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Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
                                                 285
                             280
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Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
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                         295
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
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Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
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Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
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345

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Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
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Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
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Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
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                                     410
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
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                                 425
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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
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Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
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Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
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Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
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Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
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Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
                             520
                                                 525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
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                                             540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
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                    550
                                         555
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
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gacgettegg gegtgacaga ceetgeetac gagaaacagg ttgeecaage attegeeaat
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ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac
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ggaactcctc cccgtatggt ctcagctgat cgaagagcat agccttcaag acctcaaggc
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gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggaact
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                                                                      1020
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                                                                      1440
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atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg
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ggtacgacaa aagtetgtet gggaccaaet eegegeagee taegagaaeg eeggggeeea
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                                                                      1800
gccgttcaag agtgttcatt tcgttggaac ggagacgtct ttagtttgga aagggtatat
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Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
                        55
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
                                         75
                    70
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
                85
                                     90
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
                                                     110
                                 105
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
                                                 125
                             120
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
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Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
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                                         155
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
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                                     170
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
                                 185
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
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<211> 598

<212> PRT

<213> Exophiala spinifera

<221> VARIANT

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Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
                           280
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn
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                                            300
Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
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                                        315
Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
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                                    330
Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
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Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
                           360
Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
                       375
                                            380
Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val
                   390
                                       395
Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro
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               405
Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly
           420
                               425
Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
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Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
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                                           460
Ala Arq Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys
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                                      475
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
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                                   490
Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn
                                505
           500
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
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Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
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                                            540
Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
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                                        555
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
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Ser Leu Val Pro Ala Ala
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<222> (739)...(811)
<221> intron
<222> (1134)...(1185)
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<210> 43
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<213> Rhinocladiella atrovirens

<220>
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<222> (739)...(811)

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1080

1140

1200

1260

1320

1380

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1560

1620

1680 1740

1800

1860

1920 1928

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<210> 44 <211> 591 <212> PRT <213> Rhinocladiella atrovirens

<400> 44

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135
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
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           180
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
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Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
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Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
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Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
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Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
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            260
Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
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Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg
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Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
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Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
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                325
Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
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            340
Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
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Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
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                        375
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                    390
Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
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Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
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Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
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Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
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Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
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<210> 45

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

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gacgettegg cegtgacaga ceetgeetae gagaaacagg ttgeecaage attegeeaac
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                                                                       240
                                                                       300
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ggaacteett eeegeatggt eteagetgat egaagageat agtettgaag acceeaagge
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                                                                       960
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct
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ageceaegag ateageatge ttttteteae egaetaeate aagagtgeea eeggteteag
                                                                      1080
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Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
                         55
Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
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Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
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Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
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Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
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Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
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Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
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Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
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Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe
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Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
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Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
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Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
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Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp
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Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala
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His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala
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Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
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Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
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Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
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Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
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Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys
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Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu
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Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser
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Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser
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Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr
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Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp
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Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val
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Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro
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Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe
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Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
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Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
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Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
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Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
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Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
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Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
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Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
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Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
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                                                 125
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Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
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Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
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Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
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                            200
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Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
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Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
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Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
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Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
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Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
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Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
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Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
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Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
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Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
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Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
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Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
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Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
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Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
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Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
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Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
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Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
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Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
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Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
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Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
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                                                                       144
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
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ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat
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Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa
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Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
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gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
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                                                                       384
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg
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		-	_							-		aag Lys				480
_		~	_			_	~		_			cgc Arg	_	_		528
		_	-		_		_	_				acc Thr	_			576
~	_	_				_				_	_	aag Lys 205		-		624
	_		_	_	_				_	_	_	att Ile	_			672
												aac Asn				720
					-				_			cga Arg	_		_	768
	_			_	-		_			_	_	tta Leu	-			816
_				_								gcc Ala 285		_		864
		-										aag Lys				912
_		-	_	_			_	_		-		tcg Ser				960
												acc Thr				1008
												gga Gly				1056
	_				_		_	_	_	-		aag Lys 365				1104

		ctc Leu														1152
		aac Asn														1200
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		ggt Gly													tag *	1392
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Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
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Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
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           260
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
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Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
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Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
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Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
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Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
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Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
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Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
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                        375
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
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Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
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                                   410
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
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                                                                      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg
                                                                     144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
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                                                                     192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg
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Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
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gtc g Val A	gat Asp	cga Arg	caa Gln 340	tgg Trp	tcc Ser	att Ile	acc Thr	tgt Cys 345	ttc Phe	atg Met	gtc Val	gga Gly	gac Asp 350	ccg Pro	gga Gly	1056
cgg a Arg I	aag Lys	tgg Trp 355	tcc Ser	caa Gln	cag Gln	tcc Ser	aag Lys 360	cag Gln	gta Val	cga Arg	caa Gln	aag Lys 365	tct Ser	gtc Val	tgg Trp	1104
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ccg g Pro A	gcc Ala	aac Asn	gtg Val	ctc Leu	gaa Glu 390	atc Ile	gag Glu	tgg Trp	tcg Ser	aag Lys 395	cag Gln	cag Gln	tat Tyr	ttc Phe	caa Gln 400	1200
gga g Gly A	gct Ala	ccg Pro	agc Ser	gcc Ala 405	gtc Val	tat Tyr	gly aaa	ctg Leu	aac Asn 410	gat Asp	ctc Leu	atc Ile	aca Thr	ctg Leu 415	ggt Gly	1248
tcg g Ser <i>I</i>	gcg Ala	ctc Leu	aga Arg 420	acg Thr	ccg Pro	ttc Phe	aag Lys	agt Ser 425	gtt Val	cat His	ttc Phe	gtt Val	gga Gly 430	acg Thr	gag Glu	1296
acg t	tct Ser	tta Leu 435	gtt Val	tgg Trp	aaa Lys	gly aaa	tat Tyr 440	atg Met	gaa Glu	gjå aaa	gcc Ala	ata Ile 445	cga Arg	tcg Ser	ggt Gly	1344
caa o Gln <i>i</i>	cga Arg 450	ggt Gly	gct Ala	gca Ala	gaa Glu	gtt Val 455	gtg Val	gct Ala	agc Ser	ctg Leu	gtg Val 460	cca Pro	gca Ala	gca Ala	tag *	1392
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Glu	Val	Ala 115	Ser		Leu	Ala	Glu 120	Leu		Pro	Val	Trp 125	Ser		Leu	



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                                   170
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Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
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Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
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Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
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Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr
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Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
                       295
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
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Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
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Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
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96

48



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									ctc Leu							192
									ttg Leu							240
									aat Asn 90							288
									ggt Gly							336
	-	_	_	_		_	_		ctc Leu		_					384
	_			_			_		aag Lys		_					432
									tac Tyr							480
									cag Gln 170							528
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									ttc Phe							624
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									tgt Cys 250							768
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